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<110> Maines, Mahin D.

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<150> 60/141,309

<151> 1999-06-28

<150> 60/163,223

<151> 1999-11-03

<160> 37

<170> PatentIn Ver. 2.1

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<213> Homo sapiens

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Ser Ser Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu 35 40 45

Gly Ser Ile Asp Gly Val Gln Gln Ile Ser Leu Glu Asp Ala Leu Ser 50 55 60

Ser Gln Glu Val Glu Val Ala Tyr Ile Cys Ser Glu Ser Ser Ser His 65 70 75 80

Glu Asp Tyr Ile Arg Gln Phe Leu Asn Ala Gly Lys His Val Leu Val 85 90 95

Glu Tyr Pro Met Thr Leu Ser Leu Ala Ala Ala Gln Glu Leu Trp Glu

100 105 110

Leu Ala Glu Gln Lys Gly Lys Val Leu His Glu Glu His Val Glu Leu 115 120 125

Leu Met Glu Glu Phe Ala Phe Leu Lys Lys Glu Val Val Gly Lys Asp 130 135 140

Leu Leu Lys Gly Ser Leu Leu Phe Thr Ser Asp Pro Leu Glu Glu Asp 145 150 155 160

Arg Phe Gly Phe Pro Ala Phe Ser Gly Ile Ser Arg Leu Thr Trp Leu 165 170 175

Val Ser Leu Phe Gly Glu Leu Ser Leu Val Ser Ala Thr Leu Glu Glu 180 185 190

Arg Lys Glu Asp Gln Tyr Met Lys Met Thr Val Cys Leu Glu Thr Glu
195 200 205

Lys Lys Ser Pro Leu Ser Trp Ile Glu Glu Lys Gly Pro Gly Leu Lys 210 225 220

Arg Asn Arg Tyr Leu Ser Phe His Phe Lys Ser Gly Ser Leu Glu Asn 225 230 235 240

Val Pro Asn Val Gly Val Asn Lys Asn Ile Phe Leu Lys Asp Gln Asn 245 250 255

Ile Phe Val Gln Lys Leu Leu Gly Gln Phe Ser Glu Lys Glu Leu Ala 260 265 270

Ala Glu Lys Lys Arg Ile Leu His Cys Leu Gly Leu Ala Glu Glu Ile 275 280 285

Gln Lys Tyr Cys Cys Ser Arg Lys 290 295

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<213> Homo sapiens

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20 25 30

Ser Ser Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu
35 40 45

Gly Ser Ile Asp Gly Val Gln Gln Ile Ser Leu Glu Asp Ala Leu Ser 50 55 60

Ser Gln Glu Val Glu Val Ala Tyr Ile Cys Ser Glu Ser Ser His
65 70 75 80

Glu Asp Tyr Ile Arg Gln Phe Leu Asn Ala Gly Lys His Val Leu Val
85 90 95

Glu Tyr Pro Met Thr Leu Ser Leu Ala Ala Ala Gln Glu Leu Trp Glu 100 105 110

Leu Ala Glu Gln Lys Gly Lys Val Leu His Glu Glu His Val Glu Leu 115 120 125

Leu Met Glu Glu Phe Ala Phe Leu Lys Lys Glu Val Val Gly Lys Asp

130 135 140

Leu Leu Lys Gly Ser Leu Leu Phe Thr Ala Gly Pro Leu Glu Glu 145 150 155 160

Arg Phe Gly Phe Pro Ala Phe Ser Gly Ile Ser Arg Leu Thr Trp Leu 165 170 175

Val Ser Leu Phe Gly Glu Leu Ser Leu Val Ser Ala Thr Leu Glu Glu 180 185 190

Arg Lys Glu Asp Gln Tyr Met Lys Met Thr Val Cys Leu Glu Thr Glu 195 200 205

Lys Lys Ser Pro Leu Ser Trp Ile Glu Glu Lys Gly Pro Gly Leu Lys 210 215 220

Arg Asn Arg Tyr Leu Ser Phe His Phe Lys Ser Gly Ser Leu Glu Asn 225 230 235 240

Val Pro Asn Val Gly Val Asn Lys Asn Ile Phe Leu Lys Asp Gln Asn 245 250 255

Ile Phe Val Gln Lys Leu Leu Gly Gln Phe Ser Glu Lys Glu Leu Ala 260 265 270

Ala Glu Lys Lys Arg Ile Leu His Cys Leu Gly Leu Ala Glu Glu Ile 275 280 285

Gln Lys Tyr Cys Cys Ser Arg Lys 290 295

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Ala Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu Gly 35 40 45

Ser Leu Asp Glu Val Arg Gln Ile Ser Leu Glu Asp Ala Leu Arg Ser 50 55 60

Gln Glu Ile Asp Val Ala Tyr Ile Cys Ser Glu Ser Ser His Glu
65 70 75 80

Asp Tyr Ile Arg Gln Phe Leu Gln Ala Gly Lys His Val Leu Val Glu 85 90 95

Tyr Pro Met Thr Leu Ser Phe Ala Ala Ala Gln Glu Leu Trp Glu Leu 100 105 110

Ala Ala Gln Lys Gly Arg Val Leu His Glu Glu His Val Glu Leu Leu 115 120 125

Met Glu Glu Phe Glu Phe Leu Arg Arg Glu Val Leu Gly Lys Glu Leu 130 135 140

Leu Lys Gly Ser Leu Arg Phe Thr Ala Ser Pro Leu Glu Glu Glu Arg 145 150 155 160

Phe Gly Phe Pro Ala Phe Ser Gly Ile Ser Arg Leu Thr Trp Leu Val 165 170 175

Ser Leu Phe Gly Glu Leu Ser Leu Ile Ser Ala Thr Leu Glu Glu Arg 180 185 190

Lys Glu Asp Gln Tyr Met Lys Met Thr Val Gln Leu Glu Thr Gln Asn 195 200 205

Lys Gly Leu Leu Ser Trp Ile Glu Glu Lys Gly Pro Gly Leu Lys Arg 210 215 220

Asn Arg Tyr Val Asn Phe Gln Phe Thr Ser Gly Ser Leu Glu Glu Val 225 230 235 240

Pro Ser Val Gly Val Asn Lys Asn Ile Phe Leu Lys Asp Gln Asp Ile
245 250 255

Phe Val Gln Lys Leu Leu Asp Gln Val Ser Ala Glu Asp Leu Ala Ala 260 265 270

Glu Lys Lys Arg Ile Met His Cys Leu Gly Leu Ala Ser Asp Ile Gln 275 280 285

Lys Leu Cys His Gln Lys Lys 290 295

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qaaatttgga gtggtagtgg ttggtgttgg cagagctggc tcggtgaggc tgagggactt 180
gaaggatcca cgctctgcag cattcctgaa cctgattgga tttgtgtcca gacgagagct 240
tgggagcctt gatgaagtac ggcagatttc tttggaagat gctctccgaa gccaagagat 300
tgatgtcgcc tatatttgca gtgagagttc cagccatgaa gactatatac ggcagtttct 360
graggetgge aagratgtee tegtggaata ecceatgaca etgteatttg eggeggeeca 420
ggagctgtgg gagctggccg cacagaaagg gagagtcctg catgaggagc acgtggaact 480
cttgatggag gaattcgaat tcctgagaag agaagtgttg gggaaagagc tactgaaagg 540
gtctcttcgc ttcacagcta gcccactgga agaagagaga tttggcttcc ctgcgttcag 600
eggeatttet egeetgacet ggetggtete eetetteggg gagetttete ttatttetge 660
caccttggaa gagcgaaaag aggatcagta tatgaaaatg accgtgcagc tggagaccca 720
gaacaagggt ctgctgtcat ggattgaaga gaaagggcct ggcttaaaaa gaaacagata 780
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gaacattttc ctgaaagatc aggatatatt tgttcagaag ctcttagacc aggtctctgc 900
agaggacctg gctgctgaga agaagcgcat catgcattgc ctggggctgg ccagcgacat 960
ccagaagctt tgccaccaga agaagtgaag aggaagcttc agagacttct gaagggggcc 1020
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      domain of BVR
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<222> (2)
<223> where X is any aa
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Phe Xaa Val Val Val
<210> 7
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<211> 6
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<211> 8
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<213> Artificial Sequence
<220>
<223> Description of Artificial Sequence:
      oxidoreductase domain of BVR
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  1
                  5
<210> 9
<211> 29
<212> PRT
<213> Artificial Sequence
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<221> PEPTIDE
<222> (2)
<223> where X is any aa
<400> 9
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1 5 10 15

Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Leu 20 25

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of BVR

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Pro Gly Leu Lys Arg
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<220>
<221> PEPTIDE
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<223> where X is any aa
<400> 16
Lys Lys Arg Ile Xaa His Cys
  1
                  5
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<211> 8
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<223> Description of Artificial Sequence: protein
      kinase C inhibiting domain
<220>
<221> PEPTIDE
<222> (3)
<223> where X is any aa
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Gln Lys Xaa Cys Xaa Xaa Xaa Lys
  1
                  5
<210> 18
<211> 7
<212> PRT
<213> Artificial Sequence
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<223> Description of Artificial Sequence: protein kinase C enhancer peptide of rBVR

<400> 18

Lys Lys Arg Ile Met His Cys

5

<210> 19

<211> 8

<212> PRT

<213> Artificial Sequence

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<223> Description of Artificial Sequence: protein kinase C inhibitor peptide of rBVR

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<210> 20

<211> 1014

<212> PRT

<213> Homo sapiens

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Gly Arg Ala Ser Cys Lys Lys Cys Ser Glu Ser Ile Pro Lys Asp Ser 20 25 30

Leu Arg Met Ala Ile Met Val Gln Ser Pro Met Phe Asp Gly Lys Val 35 40 45

Pro His Trp Tyr His Phe Ser Cys Phe Trp Lys Val Gly His Ser Ile
50 55 60

Arg His Pro Asp Val Glu Val Asp Gly Phe Ser Glu Leu Arg Trp Asp 65 70 75 80

Asp Gln Gln Lys Val Lys Lys Thr Ala Glu Ala Gly Gly Val Thr Gly 85 90 95

Lys Gly Gln Asp Gly Ile Gly Ser Lys Ala Glu Lys Thr Leu Gly Asp 100 105 110 Phe Ala Ala Glu Tyr Ala Lys Ser Asn Arg Ser Thr Cys Lys Gly Cys 115 120 125

Met Glu Lys Ile Glu Lys Gly Gln Val Arg Leu Ser Lys Lys Met Val 130 135 140

Asp Pro Glu Lys Pro Gln Leu Gly Met Ile Asp Arg Trp Tyr His Pro 145 150 155 160

Gly Cys Phe Val Lys Asn Arg Glu Glu Leu Gly Phe Arg Pro Glu Tyr 165 170 175

Ser Ala Ser Gln Leu Lys Gly Phe Ser Leu Leu Ala Thr Glu Asp Lys 180 185 190

Glu Ala Leu Lys Lys Gln Leu Pro Gly Val Lys Ser Glu Gly Lys Arg 195 200 205

Lys Gly Asp Glu Val Asp Gly Val Asp Glu Val Ala Lys Lys Lys Ser. 210 215 220

Lys Lys Glu Lys Asp Lys Asp Ser Lys Leu Glu Lys Ala Leu Lys Ala 225 230 235 240

Gln Asn Asp Leu Ile Trp Asn Ile Lys Asp Glu Leu Lys Lys Val Cys 245 250 255

Ser Thr Asn Asp Leu Lys Glu Leu Leu Ile Phe Asn Lys Gln Gln Val 260 265 270

Pro Ser Gly Glu Ser Ala Ile Leu Asp Arg Val Ala Asp Gly Met Val 275 280 285

Phe Gly Ala Leu Leu Pro Cys Glu Glu Cys Ser Gly Gln Leu Val Phe 290 295 300

Lys Ser Asp Ala Tyr Tyr Cys Thr Gly Asp Val Thr Ala Trp Thr Lys 305 310 315 320

Cys Met Val Lys Thr Gln Thr Pro Asn Arg Lys Glu Trp Val Thr Pro 325 330 335

Lys Glu Phe Arg Glu Ile Ser Tyr Leu Lys Lys Leu Lys Val Lys Lys 340 345 350

Gln Asp Arg Ile Phe Pro Pro Glu Thr Ser Ala Ser Val Ala Ala Thr 355 360 365 Pro Pro Pro Ser Thr Ala Ser Ala Pro Ala Ala Val Asn Ser Ser Ala 370 375 380

Ser Ala Asp Lys Pro Leu Ser Asn Met Lys Ile Leu Thr Leu Gly Lys 385 390 395 400

Leu Ser Arg Asn Lys Asp Glu Val Lys Ala Met Ile Glu Lys Leu Gly
405 410 415

Gly Lys Leu Thr Gly Thr Ala Asn Lys Ala Ser Leu Cys Ile Ser Thr 420 425 430

Lys Lys Glu Val Glu Lys Met Asn Lys Lys Met Glu Glu Val Lys Glu
435 440 445

Ala Asn Ile Arg Val Val Ser Glu Asp Phe Leu Gln Asp Val Ser Ala 450 455 460

Ser Thr Lys Ser Leu Gln Glu Leu Phe Leu Ala His Ile Leu Ser Pro 465 470 475 480

Trp Gly Ala Glu Val Lys Ala Glu Pro Val Glu Val Val Ala Pro Arg
485 490 495

Gly Lys Ser Gly Ala Ala Leu Ser Lys Lys Ser Lys Gly Gln Val Lys
500 505 510

Glu Glu Gly Ile Asn Lys Ser Glu Lys Arg Met Lys Leu Thr Leu Lys 515 520 525

Gly Gly Ala Ala Val Asp Pro Asp Ser Gly Leu Glu His Ser Ala His 530 535 540

Val Leu Glu Lys Gly Gly Lys Val Phe Ser Ala Thr Leu Gly Leu Val 545 550 555 560

Asp Ile Val Lys Gly Thr Asn Ser Tyr Tyr Lys Leu Gln Leu Leu Glu 565 570 575

Asp Asp Lys Glu Asn Arg Tyr Trp Ile Phe Arg Ser Trp Gly Arg Val 580 585 590

Gly Thr Val Ile Gly Ser Asn Lys Leu Glu Gln Met Pro Ser Lys Glu
595 600 605

Asp Ala Ile Glu His Phe Met Lys Leu Tyr Glu Glu Lys Thr Gly Asn 610 620

Ala Trp His Ser Lys Asn Phe Thr Lys Tyr Pro Lys Lys Phe Tyr Pro Leu Glu Ile Asp Tyr Gly Gln Asp Glu Glu Ala Val Lys Lys Leu Thr Val Asn Pro Gly Thr Lys Ser Lys Leu Pro Lys Pro Val Gln Asp Leu Ile Lys Met Ile Phe Asp Val Glu Ser Met Lys Lys Ala Met Val Glu Tyr Glu Ile Asp Leu Gln Lys Met Pro Leu Gly Lys Leu Ser Lys Arg Gln Ile Gln Ala Ala Tyr Ser Ile Leu Ser Glu Val Gln Gln Ala Val Ser Gln Gly Ser Ser Asp Ser Gln Ile Leu Asp Leu Ser Asn Arg Phe Tyr Thr Leu Ile Pro His Asp Phe Gly Met Lys Lys Pro Pro Leu Leu Asn Asn Ala Asp Ser Val Gln Ala Lys Val Glu Met Leu Asp Asn Leu Leu Asp Ile Glu Val Ala Tyr Ser Leu Leu Arg Gly Gly Ser Asp Asp Ser Ser Lys Asp Pro Ile Asp Val Asn Tyr Glu Lys Leu Lys Thr Asp Ile Lys Val Val Asp Arg Asp Ser Glu Glu Ala Glu Ile Ile Arg Lys Tyr Val Lys Asn Thr His Ala Thr Thr His Asn Ala Tyr Asp Leu Glu Val Ile Asp Ile Phe Lys Ile Glu Arg Glu Gly Glu Cys Gln Arg Tyr Lys Pro Phe Lys Gln Leu His Asn Arg Arg Leu Leu Trp His Gly Ser

Arg Thr Thr Asn Phe Ala Gly Ile Leu Ser Gln Gly Leu Arg Ile Ala

Pro Pro Glu Ala Pro Val Thr Gly Tyr Met Phe Gly Lys Gly Ile Tyr 885 890 895

Phe Ala Asp Met Val Ser Lys Ser Ala Asn Tyr Cys His Thr Ser Gln 900 905 910

Gly Asp Pro Ile Gly Leu Ile Leu Leu Gly Glu Val Ala Leu Gly Asn 915 920 925

Met Tyr Glu Leu Lys His Ala Ser His Ile Ser Lys Leu Pro Lys Gly 930 935 940

Lys His Ser Val Lys Gly Leu Gly Lys Thr Thr Pro Asp Pro Ser Ala 945 950 955 960

Asn Ile Ser Leu Asp Gly Val Asp Val Pro Leu Gly Thr Gly Ile Ser 965 970 975

Ser Gly Val Asn Asp Thr Ser Leu Leu Tyr Asn Glu Tyr Ile Val Tyr 980 985 990

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Phe Lys Thr Ser Leu Trp 1010

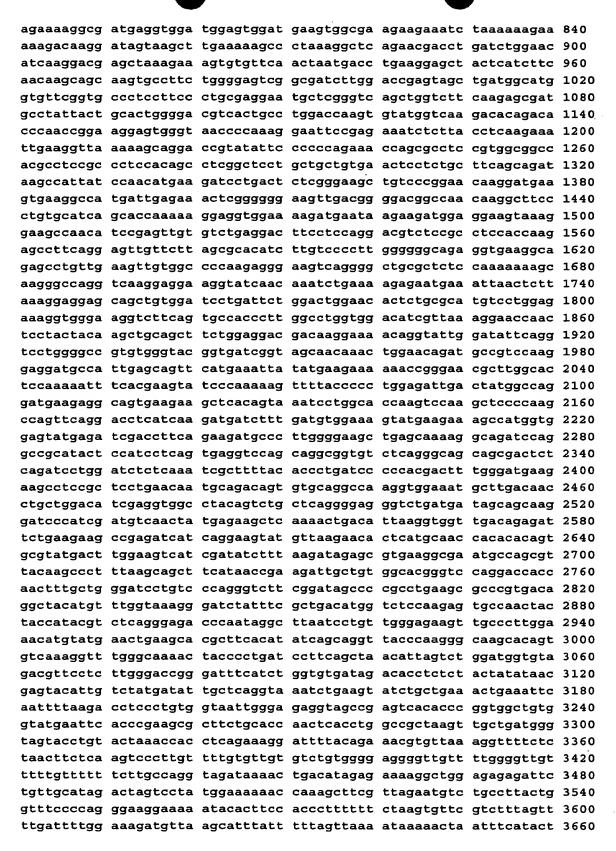
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<213> Homo sapiens

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99.009.009.00 09.009.00 9.09.00
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<211> 27 <212> DNA
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Val Ile Gly Ser Thr Gly

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      kinase C inhibitor
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